

# SEQUENCE LISTING

<110> Dhugga, Kanwarpal S.  
Niu, Xiaomu  
Helentjaris, Timothy

<120> Manipulation of Sucrose Synthase Genes  
to Improve Stalk and Grain Quality

<130> 1301

<150> 60/270,777

<151> 2001-02-22

<160> 13

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Zea mays

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<400> 2

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Gly	Ile	Leu	Gln	Pro	His	His	Ile	Leu	Asp	Ala	Leu	Asp	Glu	Val	Gln
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Arg	Ser	Ala	Gln	Glu	Ala	Ile	Val	Leu	Pro	Pro	Phe	Val	Ala	Ile	Ala
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Val	Arg	Pro	Arg	Pro	Gly	Val	Trp	Glu	Tyr	Val	Arg	Val	Asn	Val	His
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Glu	Leu	Ser	Val	Glu	Gln	Leu	Thr	Val	Ser	Glu	Tyr	Leu	Arg	Phe	Lys
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Glu	Glu	Leu	Val	Asp	Gly	Gln	His	Asn	Asp	Pro	Tyr	Val	Leu	Glu	Leu
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Asp	Phe	Glu	Pro	Phe	Asn	Val	Ser	Val	Pro	Arg	Pro	Asn	Arg	Ser	Ser
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Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu	Asn	Arg	His	Leu	Ser	Ser	Ile
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Met	Phe	Arg	Asn	Arg	Asp	Cys	Leu	Glu	Pro	Leu	Leu	Asp	Phe	Leu	Arg
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Gly	His	Arg	His	Lys	Gly	His	Val	Met	Met	Leu	Asn	Asp	Arg	Ile	Gln
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Ser	Leu	Gly	Arg	Leu	Gln	Ser	Val	Leu	Thr	Lys	Ala	Glu	Glu	His	Leu
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Gln	Glu	Trp	Gly	Leu	Glu	Lys	Gly	Trp	Gly	Asp	Thr	Ala	Gly	His	Val
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Leu	Glu	Met	Ile	His	Leu	Leu	Leu	Asp	Ile	Ile	Gln	Ala	Pro	Asp	Pro
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Ser	Thr	Leu	Glu	Lys	Phe	Leu	Gly	Arg	Ile	Pro	Met	Ile	Phe	Asn	Val
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Val	Val	Val	Ser	Pro	His	Gly	Tyr	Phe	Gly	Gln	Ala	Asn	Val	Leu	Gly
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Leu	Pro	Asp	Thr	Gly	Gly	Gln	Ile	Val	Tyr	Ile	Leu	Asp	Gln	Val	Arg

10030114-022102

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Ala Leu Glu Asn Glu Met Val Leu Arg Leu Lys Lys Gln Gly Leu Asp		
305	310	315
Val Ser Pro Lys Ile Leu Ile Val Thr Arg Leu Ile Pro Asp Ala Lys		320
	325	330
Gly Thr Ser Cys Asn Gln Arg Leu Glu Arg Ile Ser Gly Thr Gln His		335
	340	345
Thr Tyr Ile Leu Arg Val Pro Phe Arg Asn Glu Asn Gly Ile Leu Lys		350
	355	360
Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu Glu Thr Phe Ala		365
	370	375
Glu Asp Ala Ala Gly Glu Ile Ala Ala Glu Leu Gln Gly Thr Pro Asp		380
385	390	395
Phe Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu		400
	405	410
Ser Tyr Lys Met Gly Ile Thr Gln Cys Asn Ile Ala His Ala Leu Glu		415
	420	425
Lys Thr Lys Tyr Pro Asp Ser Asp Ile Phe Trp Lys Asn Phe Asp Glu		430
	435	440
Lys Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Ile Ile Ala Met Asn		445
	450	455
Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser		460
465	470	475
Lys Asn Thr Val Gly Gln Tyr Glu Ser His Thr Ala Phe Thr Leu Pro		480
	485	490
Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe		495
	500	505
Asn Ile Val Ser Pro Gly Ala Asp Met Ser Ile Tyr Phe Pro His Thr		510
	515	520
Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu		525
	530	535
Ile Tyr Asp Pro Glu Gln Asn Asp Glu His Ile Gly His Leu Asp Asp		540
545	550	555
Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg Val Lys		560
	565	570
Asn Ile Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg		575
	580	585
Glu Leu Val Asn Leu Val Val Val Ala Gly Tyr Asn Asp Val Asn Lys		590
	595	600
Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu		605
	610	615
Ile Lys Thr His Asn Leu Phe Gly Gln Phe Arg Trp Ile Ser Ala Gln		620
625	630	635
Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr		640
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His Gly Ala Phe Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr		655
	660	665
Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His		670
	675	680
Gly Gly Pro Ala Glu Ile Ile Glu His Gly Val Ser Gly Phe His Ile		685
	690	695
Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe Phe		700
705	710	715
Asp Arg Cys Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala		720
	725	730
Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile Tyr Ser Glu		735
	740	745
Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser		750

10080114-022102

755	760	765
Lys Leu Glu Arg Leu Glu Thr Arg Arg Tyr Leu Glu Met Phe Tyr Ile		
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Pro Gln		800

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 <211> 36  
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 <213> Artificial Sequence

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 <212> DNA  
 <213> Zea mays

<220>  
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                   Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu  
                   1                  5                  10

cgc ctt ggt gcc acc ttc tcc tcc cat ccc aat gaa ctg ata gca ctc 158  
 Arg Leu Gly Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu  
           15                  20                  25

ttt tcc agg tat gtt cac cag ggc aag gga atg ctt cag cgc cat cag 206  
 Phe Ser Arg Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln  
   30                  35                  40                  45

ctg ctt gcg gag ttt gat gcc ctg ttt gat agt gac aag gag aag tat 254  
 Leu Leu Ala Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr  
                   50                  55                  60

gca cca ttt gaa gac att ctt cgt gct gct cag gaa gca att gtg ctc 302  
 Ala Pro Phe Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu  
           65                  70                  75

ccc cca tgg gtt gca ctt gct atc agg cca agg cct ggt gtc tgg gat 350  
 Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp  
           80                  85                  90

tac att cgg gtg aat gta agt gag ctg gct gtg gag gag ctg agt gtt 398

10080114-022102

Tyr	Ile	Arg	Val	Asn	Val	Ser	Glu	Leu	Ala	Val	Glu	Glu	Leu	Ser	Val		
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Ser	Glu	Tyr	Leu	Ala	Phe	Lys	Glu	Gln	Leu	Val	Asp	Gly	Gln	Ser	Asn		
110					115					120					125		
agc	aac	ttt	gtg	ctt	gag	ctt	gat	ttt	gag	ccc	ttc	aat	gcc	tcc	ttt	494	
Ser	Asn	Phe	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Ala	Ser	Phe		
				130					135					140			
cct	cgt	cct	tcc	atg	tcg	aag	tcc	atc	gga	aat	gga	gtg	caa	ttc	ctt	542	
Pro	Arg	Pro	Ser	Met	Ser	Lys	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu		
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aac	cga	cac	ctg	tcg	tcc	aag	ttg	ttc	cag	gac	aag	gag	agt	ttg	tac	590	
Asn	Arg	His	Leu	Ser	Ser	Lys	Leu	Phe	Gln	Asp	Lys	Glu	Ser	Leu	Tyr		
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ccc	ttg	ctg	aac	ttc	ctc	aag	gct	cat	aac	tac	aag	ggc	acg	acg	atg	638	
Pro	Leu	Leu	Asn	Phe	Leu	Lys	Ala	His	Asn	Tyr	Lys	Gly	Thr	Thr	Met		
	175					180					185						
atg	ttg	aat	gac	aga	atc	caa	agc	ctt	cgt	ggt	ctc	caa	tca	tcc	ctg	686	
Met	Leu	Asn	Asp	Arg	Ile	Gln	Ser	Leu	Arg	Gly	Leu	Gln	Ser	Ser	Leu		
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aga	aag	gca	gag	gag	tat	cta	ctg	agt	gtt	cct	caa	gac	act	ccc	tac	734	
Arg	Lys	Ala	Glu	Glu	Tyr	Leu	Leu	Ser	Val	Pro	Gln	Asp	Thr	Pro	Tyr		
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tcg	gag	ttc	aac	cat	agg	ttc	caa	gag	ctt	ggc	ttg	gag	aag	ggg	tgg	782	
Ser	Glu	Phe	Asn	His	Arg	Phe	Gln	Glu	Leu	Gly	Leu	Glu	Lys	Gly	Trp		
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ggt	gac	act	gcg	aag	cgt	gtt	ctc	gac	aca	ctc	cac	ttg	ctt	ctc	gac	830	
Gly	Asp	Thr	Ala	Lys	Arg	Val	Leu	Asp	Thr	Leu	His	Leu	Leu	Leu	Asp		
		240				245					250						
ctt	ctt	gag	gcc	cct	gat	cct	gcc	aac	ttg	gag	aag	ttc	ctt	gga	act	878	
Leu	Leu	Glu	Ala	Pro	Asp	Pro	Ala	Asn	Leu	Glu	Lys	Phe	Leu	Gly	Thr		
		255				260					265						
ata	cca	atg	atg	ttc	aac	gtt	gtt	atc	ctg	tct	cct	cat	ggc	tac	ttc	926	
Ile	Pro	Met	Met	Phe	Asn	Val	Val	Ile	Leu	Ser	Pro	His	Gly	Tyr	Phe		
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gcc	cag	tcc	aat	gtg	ctt	gga	tac	cct	gac	act	ggc	ggt	cag	gtt	gtg	974	
Ala	Gln	Ser	Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr	Gly	Gly	Gln	Val	Val		
				290					295					300			
tac	att	ctg	gat	caa	gtc	cgt	gct	ttg	gag	aat	gag	atg	ctt	ctg	agg	1022	
Tyr	Ile	Leu	Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Leu	Leu	Arg		
			305					310					315				
att	aag	cag	caa	ggc	ctt	gat	atc	act	ccg	aag	atc	ctc	att	gtt	acc	1070	
Ile	Lys	Gln	Gln	Gly	Leu	Asp	Ile	Thr	Pro	Lys	Ile	Leu	Ile	Val	Thr		
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10050114-022402

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Arg Leu Leu Pro Asp Ala Ala Gly Thr Thr Cys Gly Gln Arg Leu Glu	
335 340 345	
aag gtc att ggt act gag cac aca gac atc att cgc gtt ccc ttc aga	1166
Lys Val Ile Gly Thr Glu His Thr Asp Ile Ile Arg Val Pro Phe Arg	
350 355 360 365	
aat gag aat ggc atc ctc cgc aag tgg atc tct cgt ttt gat gtc tgg	1214
Asn Glu Asn Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp	
370 375 380	
cca tac ctg gag aca tac act gag gat gtt tcc agt gaa ata atg aaa	1262
Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ser Ser Glu Ile Met Lys	
385 390 395	
gaa atg cag gcc aag cct gac ctt atc att ggc aac tac agc gat ggc	1310
Glu Met Gln Ala Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly	
400 405 410	
aac cta gtc gcc act ctg ctc gcg cac aag ttg gga gtc act cag tgt	1358
Asn Leu Val Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys	
415 420 425	
acc atc gct cat gcc ttg gag aaa acc aaa tac ccc aac tcg gac atc	1406
Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile	
430 435 440 445	
tac ttg gac aaa ttc gac agc cag tac cac ttc tct tgc cag ttc aca	1454
Tyr Leu Asp Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr	
450 455 460	
gct gac ctt att gcc atg aac cac acc gat ttc atc atc acc agc aca	1502
Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr	
465 470 475	
ttc caa gaa atc gcg gga agc aag gac acc gtg ggg cag tac gag tcc	1550
Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu Ser	
480 485 490	
cat atc gcg ttc act ctt cct ggg ctc tac cgt gtc gtc cat ggc atc	1598
His Ile Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile	
495 500 505	
gat gtt ttc gat ccc aag ttc aac att gtc tct cct gga gca gac atg	1646
Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met	
510 515 520 525	
agt gtt tac tac cct tat acg gaa acc gac aag aga ctc act gcc ttc	1694
Ser Val Tyr Tyr Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe	
530 535 540	
cat cct gaa atc gag gag ctc atc tac agc gac gtc gag aac tcc gag	1742
His Pro Glu Ile Glu Glu Leu Ile Tyr Ser Asp Val Glu Asn Ser Glu	
545 550 555	
cac aag ttc gtg ctg aag gac aag aag aag ccg atc atc ttc tcg atg	1790



ccg ctg tcc ttc gat tag tacggggaaa gaaggagaag aagaagaaga 2510  
 Pro Leu Ser Phe Asp \*  
 800

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 Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Ala  
 35 40 45  
 Glu Phe Asp Ala Leu Phe Asp Ser Asp Lys Glu Lys Tyr Ala Pro Phe  
 50 55 60  
 Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp  
 65 70 75 80  
 Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg  
 85 90 95  
 Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Ser Val Ser Glu Tyr  
 100 105 110  
 Leu Ala Phe Lys Glu Gln Leu Val Asp Gly Gln Ser Asn Ser Asn Phe  
 115 120 125  
 Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro  
 130 135 140  
 Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His  
 145 150 155 160  
 Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu  
 165 170 175  
 Asn Phe Leu Lys Ala His Asn Tyr Lys Gly Thr Thr Met Met Leu Asn  
 180 185 190  
 Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ser Leu Arg Lys Ala  
 195 200 205  
 Glu Glu Tyr Leu Leu Ser Val Pro Gln Asp Thr Pro Tyr Ser Glu Phe  
 210 215 220  
 Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr  
 225 230 235 240  
 Ala Lys Arg Val Leu Asp Thr Leu His Leu Leu Leu Asp Leu Leu Glu  
 245 250 255  
 Ala Pro Asp Pro Ala Asn Leu Glu Lys Phe Leu Gly Thr Ile Pro Met  
 260 265 270  
 Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser  
 275 280 285  
 Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu  
 290 295 300  
 Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln  
 305 310 315 320  
 Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu  
 325 330 335

1006014.022102



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Gly	Thr	Glu	His	Thr	Asp	Ile	Ile	Arg	Val	Pro	Phe	Arg	Asn	Glu	Asn		
		355					360					365					
Gly	Ile	Leu	Arg	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp	Pro	Tyr	Leu		
	370					375					380						
Glu	Thr	Tyr	Thr	Glu	Asp	Val	Ser	Ser	Glu	Ile	Met	Lys	Glu	Met	Gln		
385					390					395					400		
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Gly Lys Gly Met Leu Gln Pro His Gln Ile Ile Ala Glu Tyr Asn Asn  
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Lys Arg Ala Gln Glu Thr Ile His Leu Leu Leu Asp Leu Leu Glu Ala	
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Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu Pro	
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35 40 45

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Asp Ala Leu Asp Glu Val Gln Gly Ser Gly Val Arg Ala Leu Ala Glu
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Gly Pro Phe Leu Asp Val Leu Arg Ser Ala Gln Glu Ala Ile Val Leu
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Pro Pro Phe Val Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu

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His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly Ile	
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Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met	
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His Gly Ser Ile Glu Asn Leu Ile Tyr Asp Pro Glu Gln Asn Asp Glu	

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Trp Val Asn Ile Ser Gly Ala Gly Leu Gln Arg Ile Tyr Glu Lys Tyr				
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Gly Phe Trp Lys Tyr Val Ser Lys Leu Glu Arg Leu Glu Thr Arg Arg				
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Lys	Tyr	Val	Asn	Lys	Gly	Lys	Gly	Ile	Leu	Gln	Pro	His	His	Ile	Leu
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